GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	

OM nucleic - nucleic search, using sw model Run on:

August 30, 2005, 02:36:38; Search time 2069 Seconds (without alignments) 8548.165 Million cell updates/sec

US-08-731-499-9\_COPY\_10001\_10365 365 1 TITGIGGICCICCAAGGCTI.......GAIGCACICCACCACGCTIG 365 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4708233 segs, 24227607955 residues Searched:

9416466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					COLIMINALES	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	OB	ID	Description
1	365	100.0	10365	9	BD085733	BD085733 Genes fro
þ	365	100.0	121143	Φ	AF312915	AF312915 Homo sapi
3	365	100.0	128871	6	AL157838	AL157838 Human DNA
4	363.4	99.6	105023	7	AC116668	AC116668 Trypanoso
S	164	44.9	109710	σ	HSBA46E17	AL050402 Human DNA
9	159.2	43.6	165365	~	AC011959	AC011959 Homo sapi
, 0,	159.2	43.6	184851	σ	AC100809	AC100809 Homo sapi
œ	159.2	43.6	321261	ტ	AF131216	AF131216 Homo sapi
ი ა	153.8	42.1	188141	~	AC023120	AC023120 Homo sapi
10	153.4	42.0	192499	~	AC133913	AC133913 Homo sapi
11	152.6	41.8	117230	σ	HSJ684F13	AL096706 Human DNA
12	152.2	41.7	168495	~	AC084299	AC084299 Homo sapi
c 13	152	41.6	162216	~	AC136144	AC136144 Pan trogl
14	151.4	41.5	151408	~	AC010397	AC010397 Homo sapi
15	151.4	41.5	155046	~	AC146346	AC146346 Pan trogl
16	151.4	41.5	182368	~	AC145822	AC145822 Pan trogl
c 17	151.4	41.5	184010	7	AC150025	AC150025 Papio anu
c 18	151.4	41.5	196473	0	AC146345	AC146345 Pan trogl
19	151.4	41.5	253038	~	AC008930	AC008930 Homo sapi

AC112211 Homo sapi	Homo	AC027750 Homo sapi	AC025097 Homo sapi	AL672045 Human DNA	AC021189 Homo sapi	AC073342 Homo sapi	AC117502 Homo sapi	AC022160 Homo sapi	AC109516 Homo sapi	AC127024 Homo sapi	AC130324 Homo sapi	AC145842 Papio anu	AC146322 Papio anu	AC023266 Homo sapi	AC092406 Papio anu	AC145498 Papio anu	AL451140 Human DNA	AC008509 Homo sapi	AC092687 Homo sapi	AP001439 Homo sapi	AP000143 Homo sapi	Continuation (3 of	AP000090 Homo sapi	AL117338 Human DNA	AL391004 Homo sapi	
AC112211	AC104938	AC027750	AC025097	AL672045	AC021189	AC073342	AC117502	AC022160	AC109516	AC127024	AC130324	AC145842	AC146322	AC023266	AC092406	AC145498	AL451140	AC008509	AC092687	AP001439	AP000143	AC143327 2	AP000090	HSA490024	AL391004	
σ	6	~	σ	σ	N	σ	σ	~	~	σ	σ	0	~	~	σ	~	0	σ	σ	σ	σ	~	σ	6	7	
41.4 182509	.2.	41.2 170388	41.2 203530		40.9 201012	σ	40.8 104295	40.8 149202	40.8 102562	40.8 119050	40.8 153520	40.8 157502	40.8 173577	Н	40.8 192030	40.7 160099	40.7 187738	40.7 189456	40.5 189174	40.4 83661	40.4 100000	40.4 110000	7	40.4 168778	40.4 189256	
151	150.2	150.2	150.2	149.4	149.4	149.2	149	149	148.8	148.8	148.8	148.8	148.8	148.8	148.8	148.6	148.4	148.4	148	147.6	147.6	147.6	147.6	147.6	147.6	
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## ALIGNMENTS

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                                                                                                                                           10181 GATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCAGCAGC 10240
                                  10241 TGATTTTTTAAATTTTTTTTTTTGTAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCC 10300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10301 TGAGGTGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCAC 10360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF312915 13-JUN-2001
Homo sapiens chromosome 20 clones 97 and 127, complete sequence.
AF312915
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Volik,S., Collins,C., Gray,J., Wernick,M., Kowbel,D., Stultz,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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Direct Submission
Submitted (10-OCT-2000) Cancer Genetics, UCSF Cancer Center, 2340
Sutter St., Rm. 5151, San Francisco, CA 94706, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCACAGC
TITGIGGICCICCAAGGCTTACTTAACTCTGTGGGTTTAACTCTTAACCCCTGTGTATTTT
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AF312915/c
LOCUS
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AUTHORS
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JOURNAL
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97575 GATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCAGCAGC 97516
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Submitted (23-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 31, 2000 this sequence version replaced gi:9408255.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATTCTTTTGATTTGTTTTAGTCTTACTTTATTTTAGAGAAAGGGTCTTGCTCCGTCATCT 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 128871)

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0
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HTG; CpG island; zinc finger; ZNF217.
Homo sapiens (human)
Homo sapiens
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41649. .41938
                                                                                                                                                                                                                                                                                                         0; Mismatches
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Best Local Similarity 100.0%;
Matches 365; Conservative 0
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AL157838/c
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/rpt_family="Alu"
/rpt_type=dispersed
35593. .121143
/note="overlaps Homo sapiens clone RP4-724E16 on
chromosome 20 deposited in GenBank Accession Number
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/rpt_family="MBRS"
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/rpt_family="MBRS"
/rpt_type=Ai._
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/2756. .22784
/rpt_family="Alu"
/rpt_type=dispersed
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/rpt_tamily="Alu"
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                   /rpt_type=dispersed
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/rpt_family="Alu"
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complement (39791. .40072)
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/rpt_type=dispersed
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24883. .24941
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repeat: matches 5943. .6173 of consensus'
                                                                                                                                                                                                                                      1320. .7542
note="MER58B repeat: matches 117. .341 of consensus"
1545. .7838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER5A repeat: matches 4. .183 of consensus"
9580. .10108
/note="L2 repeat: matches 2622. .2747 of consensus"
10128. .10437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9606. .9733
/note="MRR33 repeat: matches 17. .148 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2550. .2709 of consensus"
14764. .14868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluJo repeat: matches 12. .299 of consensus"
5162. .15293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L2 repeat: matches 1697. .1824 of consensus"
                                                                                                                                                                                                                                                                                                      /note="AluSx repeat: matches 1. .293 of consensus"
8465. .9068
/note="match: GSS: Em:AQ386102"
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  .659. .6135
note="MER1A repeat: matches 1. .488 of consensus"
                                                                                                                                        6380. .6537
/note="79 copies 2 mer aa 60% conserved"
6658. .6567
/note="AluSg repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                          8523. .8814
/note="AluJb repeat: matches 1. .294 of consensus"
9262. .9561
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/note="Alusq repeat: matches 1, .301 of consensus"
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/note="MIR repeat: matches 63. 137 of consensus"
10781. 11083
/note="AluSx repeat: matches 1. 306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSg repeat: matches 1. .299 of consensus"
11878. .12182
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/note="MLT1G repeat: matches 3. .338 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 103. .208 of consensus"
14891. .15152
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//note="AluSc repeat: matches 1. .306 of consensus"
16610. .16901
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/nocte="MER91 repeat: matches 32. .59 of consensus"
18383. .18507
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                                            1164. .6225
/hote="31 copies 2 mer aa 71% conserved"
6245. .6379
/note="Alugg/x repeat: matches 162. .296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9562. .9599
/note="19 copies 2 mer tt 81% conserved"
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/note="match: GSS: Em:AQ499673"
complement (10991. .11319)
/note="match: GSS: Em:AQ283579"
11462. .11759
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/note="L1MB3 1
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/note="MLTIC
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The following abbreviations are used to associate primary accession undbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORWPEP; Information on the WORMPEP database can be found at
                                                                                                                                                         Mapping Group.

Http://www.sanger.ac.uk/HGP/Chr20

This sequence is the entire insert of clone RP4-724E16 The true right end of clone RP5-823G15 is at 19684 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-724816 is from the library RPCI-4 constructed by the group of Pieter de Jong. For
                                                                                    http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1308. .3436
//note="LiMA4 repeat: matches 6162. .6293 of consensus"
3455. .3551
//note="WEREA repeat: matches 61. .183 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        872. .3026 note="LiMA4 repeat: matches 6017. .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .54
"note="MLT2A repeat: matches 362. .415 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluSq repeat: matches 126. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              871. .4004
note="AluSq/x repeat: matches 1. .134 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564. 3697
note="MER5B repeat: matches 14. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5492. .5648
/note="L2 repeat: matches 2589. .2745 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .137. 1270
note="FLAM_C repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415. 1709
note="AluJo repeat: matches 14. .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note="WERSA repeat: matches 4. .189 of consensus"
2806. .2870
note="WERSA repeat: matches 10. .75 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is. .368
'note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       027. .3307
note="AluJo repeat: matches 1. .290 of consensus"
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note="AluSx repeat: matches 1. .297 of consensus"
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note="AluSc repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             948. .2041
note≈"MER5A repeat: matches 6. .101 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744. 1902
note="MIR repeat: matches 14. .175 of consensus"
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/note="match: GSS: Em:AQ261624"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .871. .2326
'note="match: GSS: Em:AQ673688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type="genomic_DNA"
xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="20"
/map="q13.12-13.32"
/clone="RP4-724E16"
/clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/note="13 cc
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.292 of consensus"

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

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                                                                                                                                                                                                                                                                                                                                                        20689. .20814
/noce="FLAM A repeat: matches 14. .136 of consensus"
20816. .21218
/note="Charlie4a repeat: matches 17. .427 of consensus"
                                                                                                                                                                                                                                                                                             ATTCTTTTGATTTGTTTAGTCTTACTTTATTTTAGAGAAAAGGGTCTTGCTCGTCATCT
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                                                                        18835. .19184
/note="THEIA repeat: matches 1. .354 of consensus"
19211. .19522
/note="match: STS: Em:HSA153YF5"
19297. .19346
/note="25 copies 2 mer ca 100% conserved"
194564. .19564
/note="Matches 6. .147 of consensus"
19624. .19916
/note="Alusx repeat: matches 1. .295 of consensus"
                                .261 of consensus"
                                                                                                                                                                                                                                             note="MER20 repeat: matches 1. .218 of consensus" (0215. .20317
                                                                                                                                                                                                                                                                             note="MER5A repeat: matches 4. .108 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                    21337. .21634
/note="AluY repeat: matches 1. .297 of consensus"
'note="MIR repeat: matches 23. .148 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 365; DB 9; Length 128871; 100.0%; Pred. No. 3.4e-90;
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                           note="wir repeat: matches 137. .261 of c 18799. .18820
note="11 copies 2 mer aa 100% conserved"
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Trypanosoma.

I (basea 1 to 105023)

El-Sayed, M.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K.,
Peterson, J., Hou, L., Zhao, H., Mason, T., Militscher, J., Pai, G., Van
Aken, S., Utterback, T., Khalak, H.G., Gerard, C., Leech, V., Ullu, E.,
Melville, S., White, O., Adams, W. D., Donelson, J. E. and Fraser, C. M.
Trypanosoma brucei GUTatlo.1 RPC193-45E22 BAC genomic sequence
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E1-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

Submitted (02-ARP-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

E3 (Dasse 1 to 105023)

Submitted (01-MAY-2002) The Institute for Genomic Research, 9712

B1-Sayed, N.M., Khalak, H. and Adams, M.D.

Direct Submission

Submitted (01-MAY-2002) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

On May 1, 2002 this sequence version replaced gi:20340472.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* trus of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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'Organisme"Trypanosoma brucei"

/mol type="genomic DNA"

/isolate="GUTat10.1"

/db xref="taxon:5691"

/chromosome="V"

/clone="RPCI93-45E22"
                                                                                                                                                                                                 Unpublished
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HTG 01-MAY-2002 \*\*\* SEQUENCING

Trypanosoma brucei chromosome V clone RPC193-45E22, IN PROGRESS \*\*\*, 3 unordered pieces. AC116668 AC116668.5 GI:20376999
HTG; HTGS\_PHASE1.
Trypanosoma brucei

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

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/note="L1PA5 repeat: matches 5861. .6143 of consensus"
37097. .37433
/note="match: GSS: Em:AQ136413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .5875 of consensus"
note="MER45 repeat: matches 83. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             consensus,"
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note="MER45 repeat: matches 1. .83 of consensus"
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/note="match: STS: Em. 608153"
complement (62314. .62461)
/note="match: GSS: Em.AQ744114"
complement (join) (62322. .62499,79689. .79824))
/note="match: STS: Em.Li30312"
join (62324. .62452,76137. .76341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24162. .24201
hote="20" copies 2 mer gt 92% conserved"
30439. .30918
/note="match: GSS: Em:AQ709314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="28 copies 2 mer ag 96% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 5819.
                                                                                                                                                                                                                            complement (17350. .17747)
/note="match: GSS: Em:AQS34637"
complement (17374. .17760)
/note="match: GSS: Em:AQ179064"
17772. .18403
/note="match: GSS: Em:AQ508370"
17795. .18238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: G2165)
/note="match: GSS: Em:AL253608"
/note="match: G2196
                                                                    13423. .13654
/note="match: GSS: Em:AQ490130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (62073. .62436)
/note="match: GSS: Em:AL003813"
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/note="match: GSS: Em:AL001671"
                                                                                                                complement(14203. .14663)
/note="match: GSS: Em:AQ613979"
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                                                                                                                                                                                          Em: G50283
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                                                                                                                                                                 14712. .15061
/note="match: STS:
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complement(62073. .
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34817. .35099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on the Worker's database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence as, constructed by the Sanger Centre Chromosome 22, human chromosome 22, constructed by the Sanger Centre Chromosome 22 http://www.sanger.ac.uk/HGP/Chr22 http://www.sanger.ac.uk/HGP/Chr22 http://www.chori.org/Pacpac/home.htm
VECTOR: pager.ac.uk/HGP/Chr22 http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 6, 1999 this sequence version replaced gi:5791503.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations are found these are annotated as variation are rogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emm., EMBL; Sw., SWISSPROT; Tr., TREMBL; WORNDEP, Information on the WORMPEP database can be found at
                                                                                                                   HSBA46E17 109710 bp DNA linear PRI 02-DEC-2000
Human DNA sequence from clone RP11-46E17 on chromosome 22, complete
                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 109710)
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/note="11MB5 repeat: matches 5577. .6034 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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103. .416
'note="AluSg1 repeat: matches 1. .306 of consensus"
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/note="MER45 repeat: matches 1. .120 of consensus"
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/note="18 copies 2 mer tc 94% conserved"
11101. ,11201
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/note="match: GSS: Em:AQ900161"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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165365 bp DNA linear HTG 20-APR-2000
Homo sapiens clone RP11-110L10, WORKING DRAFT SEQUENCE, 16
unoxidered pieces.
-----GITGCCCAGGCTGGTCTTGAACTCC 295
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165365)
                                                                                   GCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCACGCTGATTTTTA
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HTG; HTGS PHASEI; HTGS DRAFT.
HOMO sapiens (human)
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1455 ACCATGCTCG 1464
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/note="MER45 repeat: matches 10. .123 of consensus"
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/note="match: 57S: Em:G05108"
/note="match: STS: Em:G05108"
/note="match: STS: Em:288547"
/note="match: STS: Em:288547"
/note="match: STS: Em:207969"
complement (join (62424 . 62712,80207 . 80531))
/note="match: STS: Em:AL193675"
/note="match: STS: Em:AL193675"
/note="match: STS: Em:G08976"
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'note="match: GSS: Em:AL129551 Em:AL129826"
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complement (62344. .62470)

/note="match: GSS: Em:AL273514"

complement (62373. .62507)
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join(62385. .62479,80291. .80469)
/note="match: STS: Em:AU029014"
62389. .62503
/note="match: GSS: Em:AL268743"
complement(62390. .62608)
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/3296. 62538
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2336. .62509
                                                                                                          'note="match: GSS: Em:AQ972678"
52334. .62463
'note="match: GSS: Em:AL130784"
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complement(62336. .62530)
                                                                                                                                                                                        .2335. .62469
'note="match: GSS: Em:AL201275"
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                                                                                                                                                                                                                                              omplement (62335. .62462)
note="match: STS: Em:G15757"
                                                /note="match: STS: Em:G08433"
62334. ,62586
  'note="match: STS: Em:L18062"
                                                                                                                                                                                                                                                                                                                                  note="Tandem repeat"
                               complement (62332.
                                                                                                                                                                                                                                                 complement (62335
                                                                                                                                                                                                                                                                                                                                                                  62336. .62540
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Best Local Similarity 67.8
Matches 251; Conservative
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center project Information
Center project name: 1,2302
Center clone name: 110 L.10
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Web site: http://www-seq.wi.mit.edu
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130 TGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCT 189

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                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
   Insert size: 185000; agarose-fp
Insert size: 163865; sum-of-contigs
Quality coverage: 2.8 in Q20 bases; agarose-fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs
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contig of 8019 bp in length

contig of 8019 bp in length

contig of 6892 bp in length

contig of 100 bp

contig of 10141 bp in length

gap of 100 bp
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/note="assembly_fragment
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Homo sapiens chromosome 8, clone CTC-493P15, complete sequence.
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Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone CTC-493P15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53984 TAGCTAATTITITAAAACTTITTTTATAGAGATGGGGTTGCCCCGGCTGATCTTGAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 TITATICITITGATITGTTTAGTCTTACTITATTTTAGAGAAAGGGTCTTGCTCCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64164 TCfrtfrfrfrgrrfrgrrfrgrrgrrgrrgrrgrrgrrgrgadacagggrcrrgrca
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AC100809.9 GI:26553405
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Seeser, Jac Charles Street, Cambridge, MA 02141, USA
Birren, B., Nubbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Caok, A., Coke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Chang, J., Kellan, C., Landers, T., Levine, R., Jones, C., McCarth, M., Mellen, M., Illiev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, G., MacLean, C., Macdran, C., Macdran, C., McCarth, M., Meldrim, J., Monneus, L., Mihova, T., Matna, A., Kararas, A., Kararas, A., Kararas, D., McCarth, M., Meldrim, J., Monneus, L., Mihova, T., Matthews, C., McCarth, M., Maldrim, J., Monnell, P., O'Neil, D., Oilver, J., Petereon, K., Phunkhang, P., Petere, N., Schanger, S., Gotuback, R., Saman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Schupack, R., Saman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Schupack, R., Saman, S., Severy, P., Smith, C., Spencer, B., Stange-Thoman, N., Schupack, R., Volag, M., Milson, B., Wuyan, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M. Wyann, D., Young, G., Zainoun, J., Zemper, B., Stange-Thoman, M., Schupack, R., Coke, R., Coke, P., Datz, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, M., Bastilan, V., Chazaro, B., Chopell, Y., Collymor, T., Gardyna, S., Gord, S., Cerland, M., Gage, D., Galagan, J., Gardyna, S., Severy, P., Salion, T., Bogge, D., Galagan, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meller, W., Thiever, J., Matthews, C., McCarthy, M., Meller, W., Schubback, T., Lindback, T., Lindback, T., Lindback, T., Lander, T., Lettaer, R., Waratae, J., Tesfaye, S., Theodore, J., Tophan, K., Razatae, M., Vasatilee, W., Mayn, M., Mayn, D., Young, G., Zainoun, J., Tesfaye, S., Theodore, J., Tophan, K., Rase, L., Matthews, C., McCarthy, M., Matthews, C., McCarthy, M., Matthews, C., McCarthy, M., Matt
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petersenon, K., Phunkhang, P., Pierre, N., Pollara, V., Raymon, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, N., Subramanian, A., Talamas, J., Trefaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Aller, J., Zalmoun, J., Zalmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 12, 2002 this sequence version replaced gi:24757047.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 493_P_15
                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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Location/Qualifiers

source

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Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
Contact: gscj-submit@genome.imb-jena.de
Contact: gscj-submit@genome.imb-jena.de
Conter project name: H3WZ, H4WZ, H6WZ, H6WZ, H8WZ, H8WZ, Center clone name: CTC-433P15, CTB-31N18, CTB-164D9,
CTB-16905, CTB-65D4, CTC-271023, CTC-367124
CTB-16905, CTB-65D4, CTC-271023, CTC-367124
Sequencing vector: pUC18; 1108
Sequencing vector: pUC18; 1008
Sequencing vector: pUC18; 1008 of reads
Chemistry: Dye-terminacy Big Dye; 1008 of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 319678 bases at least Q40
Consensus quality: 321261 bases at least Q20
Quality coverage: 16.24x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                    Submitted (25-FEB-1999) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 321261) Lagemann, D. and Platzer, M. Direct Submission
                                                                                                                                                                                                                                                                               Submitted (16-FRB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany On Feb 16, 2004 this sequence version replaced gi:8272458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="8 map 8p23-p22"
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CTC-367J24, complete sequence, and clones CTC-493P15,
CTB-31N18, partial sequence."
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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Center: Insitute of Molecular Biotechnology
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/db_xref="taxon:9606"
                       Chromosome 8 genomic sequence
Unpublished
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                                                                                               Reichwald, K. and Platzer, M. Direct Submission
                                                                             (bases 1 to 321261)
                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: IMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14838 rccAdgcrddAardCAGrddcAaArCArAGCrCACrdcAacCardGArrcCrdAGCrCA 14779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14718 TAGCTAATTTTTAAAACTTTTTTATAGAGATGGGGTTGCCCCGGCTGATCTTGAACTCCT 14659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14658 GGGCTCAAGTGTTTCCCCTGCCTCAGCCTCCAAAGTGCTGGGATTACAGGCATGAACCA 14599
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321261 bp DNA linear PRI 16-FEB-2004

Homo sapiens chromosome 8 map 8p23-p22 clone CTB-164D9, CTB-16905,
CTB-65D4, CTC-271023, CTC-367J24, complete sequence; and clones
CTC-493P15, CTB-91N18, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AGAGATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGC-TGCTACCATGCA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 CAGCTGATTTTTAAATTTTTTTTTTTTAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GGCCTGAGGTGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 TCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 321261)
Appel,S., Reichwald,K., Hennies,H.-C., Zimmermann,W., Reis,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ITTATICITITGATITGITIAGICITIACITITATITITAGAGAAAGGGICTIGCICCGICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                       ....e="PCR product only region."
8408. .8428
/rpt_family="(CA)n"
8436. .853°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="<30 qual SNGL region."
complement(10895. 11201)
/rpt family="MER67B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 159.2; DB 9
Pred. No. 2.8e-33;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="<30 qual SNGL region."
[1353. .11472
                                                                                                                                                                                                                                                                                                                                                                                    complement (10313. 10590)
/rpt family="MER67B"
complement (10591. 10894)
/rpt family="AluSq"
                                                                                                                                                                               /rpt_family="LIMC4"
complement (9212. .9325)
/rpt_family="MIR3"
/rpt_family="(TATG)n"
complement(8007. .8407)
/rpt_family="MSTA"
8015. .8231
                                                                                                                                                                                                                                                                                                                 family="MER31A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MER5A"
11473. .11794
                                                                                                                                                                                                                                                                                                                                                                    family="(TG)n"
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AF131216.2 GI:42557499
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Best Local Similarity
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AF131216
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SOURCE
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	/clone="CTB-164D9"	/note="G substituted in clone: CTC-493P15"
Bource	72368154799 /organism="Homo ganiens"	= 0.00
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	131790/7910 /organisms"Homo sapiens" /mol type="genomic DNA"	
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	/ J. D. T. P. D.	
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variation	11751176 /note="deleted in clone: CTC-493P15"	<pre>/note="C substituted in clone: CTC-493P15" /replace="t"</pre>
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	/note="T substituted in clone: CTC-493P15" /replace="C"	
variation	3730 /note="G substituted in clone: CTC-493P15"	/note="G substituted in clone: CTC-493P15" /replace="a"
variation	" "C "	<pre>variation</pre>
	/note="T substituted in clone: CTC-493P15" /replace="C"	
variation	6772 /anterna substituted in clame, One-402018	
	מתסכידנתנכת זוו כנסופ: "g"	variation 1402-9 variation /nre-maken in clone. CTC-A02D15"
	Jose "T substituted in clone: CTC-493P15"	/moce= 1 substituted in croise: crc 1/31 / replace="0"
variation		<pre>variation 1403/ /note="A substituted in clone: CTC-493P15"</pre>
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variation	7657 /note="C substituted in clone: CTC-493P15"	tch 43.6%; Score 159.2; DB 9; al Similarity 72.4%; Pred. No. 2.8e-33;
variation	"g" 737	Matches 220; Conservative 0; Mismatches 83; Indels 1; Gaps 1;
	/note="deleted in clone: CTC-493P15"	Qy 58 ITTATICTITIGATITICTITIAGTCTTACTITIATITITIAGAGAAAGGGTCTTGCTCCGTCA 117
variation	4	Db 57470 TCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAGACAGGGTCTTGCTCTGTCA 57529
	/noce="C Bubstituted in cione: CiC-493Fi5" /replace="g"	Qy 118 TCTAGATTGGAGTGTAAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCA 177
variación	\note="A substituted in clone: CTB-91N18 , CTB-164D9" \range \range \text{TR-164D9}	Db 57530 TCCAGGCTGGAATGCAGAGCACAATCATAGCTGCACCATGGATTCCTGAGCTCA 57589
variation	/ Action 9 9 9096 / Action 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Qy 178 AGAGATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGC-TGCTACCATGCA 236
1000	י"כ"	Db 57590 AGCAATCCTCCTGCCTCCTGAGTAGCTGGGACTAGAGCTGCACCACCACCACC 57649
	/note="T substituted in clone: CTC-493P15" /renlare="C"	Qy 237 CAGCTGATTTTTTAAATTTTTTTTTTAGAGTTGCAGGCTGGTCTTGAACTCCT 296
variation	7	Db 57650 radciaatititiaaacitititatadadatedegettececedecteatetreaaciteet 57709
noiteirev	swellured in clone:	Qy 297 GGCCTGAGGTGATCCTCCTGGGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCA 356
***********	Totals /note="A substituted in clone: CTC-493P15" /rohlare="F"	Db 57710 GGGCTCAAGTGTTTCCCCTGCCTCCCAAAGTGCTGGGATTACAGGCATGAACCA 57769
variation	ס משיט מתניון משט ימייון ביין במיייון אינ	Qy 357 CCAC 360
variation	Bubberreded III CIOINE: CIB-104D9 /	Db 57770 CCAC 57773
	/note="T substituted in clone: CTB-164D9 , CTB-91N18" /replace="a"	RESULT 9
variation	10435	AC023120/c

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34291 Trirririciriricrirrircririrrirrirrirririririririririsadacardoricacic 34232
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Homo sapiens chromosome 16 clone CTD-2312J12, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 CICCIGGCCIGAGGIGAICCICCIGGGIIGACCICCCAAGIAICITAGACIACAGAIGCA 351
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1 (bass 1 to 19249)
DOB Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                       113 CGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AIGCACAGCTGAITTITAAAITTITTTTTTTAGAGAIGGAGTTGCCCAGGCTGGTCTTGAA
                                                                                                                                                                                                                Query Match 42.1%; Score 153.8; DB 2; Length 188141; Best Local Similarity 71.1%; Pred. No. 8.7e-32; Matches 217; Conservative 0; Mismatches 87; Indels 1;
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
HOmo sapiens (human)
                               29173. ... 80487
/note="assembly_name:Contig4"
80588. ..132881
                                                                                                   /note="assembly_name:Contigs"
132982. .188141
/note="assembly_name:Contig6"
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Center clone name: CITB-H1_2312J12
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Unpublished 2 (bases 1 to 192499)
DOE Joint Genome Institute.
Direct Submission
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Center Code: JGI
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29173. ..80487
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                                 misc_feature
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ACO23120
Homo sapiens chromosome 15 clone RP11-291C5, WORKING DRAFT
ACOUNTY, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H.
Direct Submission
Submitsed (08-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7107585.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 188141)
Waterston, R.H.
The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 185645 bases at least Q40
Consensus quality: 186911 bases at least Q30
Consensus quality: 186911 bases at least Q30
Insert size: 197000; agarose-fp
Insert size: 197700; agarose-fp
Unality coverage: 6.89 in Q20 bases; sum-of-contigs
Quality coverage: 7.25 in Q20 bases; sum-of-contigs
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vector_side:right"
7386._29072
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/note="assembly_name:Contig2
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                   AC023120.3 GI:7230963
HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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          Quality coverage: 19.36 in Q20 bases; agarcse-fp estimation Quality coverage: 7.06 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft" sequence. It currently consists of 7 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Pred. No. 1.1e-31;
0; Mismatches 86; Indels 15;
Estimated insert size: 191899; sum-of-contigs estimation
                                                                                                                                                                                                                                                                   2449: contig of 2449 bp in length
2450 2549: gap of unknown length
0499: contig of 7949 bp in length
0499: 10598: gap of unknown length
0599 19985: contig of 9387 bp in length
0599 19985: contig of 9387 bp in length
0686 32520: contig of 12435 bp in length
0686 32520: contig of 12435 bp in length
0686 3550: gap of unknown length
05537 45536: contig of 12916 bp in length
05637 81480: contig of 135844 bp in length
1481 192499: contig of unknown length
1581 192499: contig of unknown length
1581 192499: contig of 110919 bp in length
1581 192499: contig of 110919 bp in length.
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/clone_lib="CalTech human BAC library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/db_xref="taxon:9606"
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Best Local Similarity 69.5
Matches 230; Conservative
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HSJ684F13 117230 bp DNA linear PRI 31-OCT-2002 Human DNA sequence from clone RP4-684F13 on chromosome 10, complete

Bequence. AL096706 AL096706.10 GI:5869928

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 11 HSJ684F13 (human)

Homo sapiens Homo sapiens

ORGANISM

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded ox sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature cable with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9792 TIGIGATICITIAAICTAIGCÍAAAGTAÍCCACICAAAATÍCAÍTIGATATÍTÍCÍTÍTÍT 9851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 ATCCTTCTGCCTCCAGCTTCCCAGGTAGCTGAGACTATATGTG-CTGCTACCATGCACAGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 FA4-664F13 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 117230)
                                                                                                                            Direct Submission
Submitted (31-0CT-2002) Wellcome Trust Sanger Institute, Hinxton,
Submitted (31-0CT-2002) Wellcome Trust Sanger Institute, Hinxton,
Submitted (31-0CT-2002) Wellcome Institute:
Inimguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 10, 1999 this sequence version replaced gi:5823996.
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/db_xref="taxon:9606"
/chronosome="10"
/clone="RP4-684F13"
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41.8%; Score 152.6; DB 9
Best Local Similarity 67.0%; Pred. No. 1.9e-31;
Matches 250; Conservative 0; Mismatches 114
                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                        REFERENCE
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78448: contig of 10466 bp in length 78448: contig of 10461 bp in length 95469: contig of 16421 bp in length 95569: gap of unknown length 110500: gap of unknown length 110550: gap of unknown length 125387: contig of 14887 bp in length 125387: contig of 14887 bp in length 146498: contig of 21011 bp in length 146498: contig of 21011 bp in length 166495: contig of 21897 bp in length
                                                                                                                                                                                                   contig of 10221 bp in length gap of unknown length contig of 8203 bp in length contig of 8275 bp in length contig of 8275 bp in length gap of unknown length contig of 10656 bp in length gap of unknown length gap of unknown length
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contig of 2977 bp in length
gap of unknown length
contig of 5768 bp in length
gap of unknown length
contig of 8227 bp in length
gap of unknown length
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41049. .49251
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146599. .168495
/note="assembly_name:Contig33"
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/note="assembly_name:Contig16"
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110501. .125387
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.25488. .146498
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/note="assembly_name:Contig21"
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22401. .30627
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/note="assembly_name:Contig27"
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/db_xref="taxon:9606"
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10092 TCCTGGCCTCAGGTGATCCACCTGCCTTGGCCCCCCAAAGTGCTGGATTACAGGTGTGA 10151
                                                                                                                                                                                                                                                                                                                                                    ACO84299 168495 bp DNA linear HTG 22-OCT-2000 Homo sapiens chromosome 7 clone RP11-374D24, WORKING DRAFT SEQUENCE, 19 unordered pieces.
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Direct Submission
Direct Submission
University School of Medicine, 4444 Forest Parkway, St. Louis, Mo 63108, USA
                                                                                293 TCCTGGCCTGAGGTGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168495)
Waterston,R.H.
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Website State 
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Center code: WUGSC
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1383: gap of unknown length
3518: contig of 2015 bp in length
3518: gap of unknown length
5659: contig of 2141 bp in length
7665: contig of 1906 bp in length
7765: contig of 1906 bp in length
10469: contig of 2704 bp in length
10469: contig of unknown length
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Unpublished
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HTG; HTGS PHASE1; HTGS DRAFT.
HOMO SADIENS (human)
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38731 AGTICAAGCGAITCICCTGCCTCAGCCTCCGAGTAGCTGGGACTACAGGCGCGCACACC 38672
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Homo sapiens chromosome 5 clone CTD-2122L23, WORKING DRAFT
SEQUENCE, 9 ordered pieces.
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Unpublished
2 (Desson 1 to 151408)
DOE Joint Genome Institute.
Durect Submission
Submitted (15-589-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On May 6, 2000 this sequence version replaced gi:7710717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 CCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTG 171
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1 (bases 1 to 151408)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                     1. .162216
/organism="pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:5598"
/clone="rp43-47ml8"
/clone="rp43-47ml8"
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1 7544: contig of 7544 bp in length 7545 21317: contig of 15673 bp in length 2311. contig of 15673 bp in length 3418 102290: contig of 78873 bp in length 2291 102390: gap of unknown length 2495 113294: gap of unknown length 2495 113294: gap of unknown length 2595 102216: contig of 30104 bp in length 2595 102216: contig of 29622 bp in length 11. 162216
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Center Code: JGI
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HTG; HTGS PHASE2; HTGS_DRAFT.
HOMO sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC136144 162216 bp DNA linear HTG 01-OCT-2004 Pan troglodytes clone rp43-47m18, WORKING DRAFT SEQUENCE, 5 ordered
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                                                                                                                                                                                                                    113 CGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGA 172
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1 (bases 1 to 162216)
Lau, C. and Roe, B.A.
Lau, C. and Roe, B.A.
Uppublished
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Lau,C. and Roe, B.A.
Liect Submission
Submitted (29-0CT-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman.
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                                                                                                                                                                                                                                                                                                                                                                                                   ATGCACACCCCGGTTTTTTAAATTTTTTTTTTGAGATGGAGTTGCCCCAGGCTGGTCTTGAA
                                                                                                                          TGTATTTTATTCTTTTGATTTGTTTAGTCTTACTTTTATTTTAGAGAAAGGGTCTTGCTC
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                                                                                Gaps
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                     Length 168495;
                                                                             88; Indels
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The University Of Oklahoma
                                   DB 2;
                                 41.7%; Score 152.2; DB 2
70.8%; Pred. No. 2.4e-31;
ive 0; Mismatches 88
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HTG; HTGS PHASE2; HTGS DRAFT.
Pan troglodytes (chimpanzee)
Pan troglodytes
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3 (bases 1 to 162216)
Lau, C. and Roe, B.A.
Direct Submission
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                                                                             216; Conservative
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                                                        Similarity
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AL140346 12-AUG-2003
Pan troglodytes clone rp43-26h17, WORKING DRAFT SEQUENCE, 46
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
I (bases I to 155046)
Li,J. and Roe,B.A.
Pan troglodytes BAC Clone rp43-26h17
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Consensus quality: 146291 bases at least Q30
Consensus quality: 146291 bases at least Q30
Consensus quality: 148789 bases at least Q30
Consensus quality: 148789 bases at least Q30
Estimated insert size: 150608; sum-of-contigs estimation
Quality coverage: 6.06 in Q20 bases; pulse field gel estimation
Quality coverage: 5.78 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
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* This sequence will be preserved.

* This sequence will be preserved.

* 52908 contig of 52908 bp in length

* 52909 53008: contig of 52908 bp in length

* 53009 74920: contig of 21912 bp in length

* 75021 78508: gap of unknown length

* 75021 78508: contig of 5488 bp in length

* 75021 78508: contig of 554 bp in length

* 7609 78608: gap of unknown length

* 78509 78608: gap of unknown length

* 84263 84262: contig of 5654 bp in length

* 84263 109884: contig of 5654 bp in length

* 109885 109884: contig of 5852 bp in length

* 117979: contig of 7995 bp in length

* 117980 118079: gap of unknown length

* 118080 120817: contig of 7398 bp in length

* 120818 120917: contig of 2738 bp in length

* 140302 140401: gap of unknown length

* 140302 140401: gap of unknown length

* 140302 150408: contig of 19384 bp in length

* 140302 151408: contig of 1007 bp in length
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0; Mismatches 81; Indels 9; (
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Matches 229; Conservative
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43163: Ortrig of 2105 bp in length 40661: Contig of 2798 bp in length 46161: gap of unknown length 46161: gap of unknown length 46161: gap of unknown length 4620: contig of 2359 bp in length 4620: gap of unknown length 1620: gap of unknown length 15181: gap of unknown length 15181: gap of unknown length 15185: contig of 2394 bp in length 15185: contig of 2394 bp in length 15185: contig of 2308 bp in length 15185: contig of 2446 bp in length 15185: contig of 2680 bp in length 16193: gap of unknown length 16193: gap of unknown length 16193: contig of 268 bp in length 16193: gap of unknown length 16190: contig of 288 bp in length 16190: contig of 288 bp in length 16190: contig of 288 bp in length 16190: contig of 3129 bp in length 16190: contig of 3120 bp in length 16190: contig of 3120 bp in length 16190: contig of 3120 bp in length 16190: contig of 4663 bp in length 16191: gap of unknown length 16191: contig of 4863 bp in length 16199: contig of 4863 bp in length 16199: contig of 4863 bp in length 16191: contig of 4869 bp in length 16191: gap of unknown length 16199: contig of 480 bp in length 16199: contig of 6220 bp in length 16199: contig of 6220 bp in length 16191: gap of unknown length 16199: contig of 6220 bp in length 16199: contig
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131914: gap of unknown length
138652: contig of 6738 bp in length
138752: gap of unknown length
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12 145791: gap of unknown length
12 155046: contig of 9255 bp in length.
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30-JUN-2000;
07-JUL-2000;
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Aad58279 Human tum
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Aak78729 Human imm
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1 TTTGTGGTCCTCCAAGGCTT.....GATGCACTCCACCACGCTTG
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DE:	Humai	ı immur	ıe/hae	matopoie	tic	Human immune/haematopoietic antigen genomic sequence	e SEQ ID NO:35905.
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.

17-JAN-2001; 2001WO-US001354

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17-NOV-2000;
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 35905; 3071pp + Sequence Listing; English.

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cupplement the patients own production of (I). Additionally, (I) or supplement the patients own production of (I). Additionally, (I) cucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention

Sequence 14906 BP; 3959 A; 3088 C; 3333 G; 4526 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
                                                                                                                                                                    GATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCACAGCAGC
                                                    TTTGTGGTCCTCCAAGGCTTACTTAACTCTGTGGGTTTAACTCTTAACCCTGTGTATTTT
                                                                                                                 AGATTGGAGTGCAGCGGTGTAATCATACCTTACTGTAGTCTTGAATTCCTGAGTTCAAGA
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                                                                           ATTCTTTTGATTTGTTTAGTCTTACTTTATTTTAGAGAAAGGGTCTTGCTCCGTCATCT
                                                                                               6464 ATTCTTTTGAFTTGTTTAGTCTTTACTTTTTTAGAGAAAGGGTCTTGCTCCGTCATCT
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                                     1 TITGIGGICCTCCAAGGCTTACTTAACTCTGTGGGTTTAACTCTTTAACCCTGTGTATTTT
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Length 14906;
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                  Indels
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Score 365; DB 4;
Pred. No. 3.4e-88;
                   Mismatches
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                                                                                                                                                                                                                                                                                                                                              ACN44986 standard; DNA; 36022 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        Human genomic sequence hCG37127
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                  Conservative
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         Similarity
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                   365;
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carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a blochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TITGIGGICCTCCAAGGCTTACTTAACTCTGTGGGTTTAACTCTTAACCTGTGTATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17531 TTTGTGGTCCTCCAAGGCTTACTTAACTCTGTGGGTTTAACTCTTAACCCTGTGTATTTT
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                                                                                                                                                                                                                                             Sequence 36022 BP; 9645 A; 7326 C; 8145 G; 10906 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       Length 36022;
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                                                                                                                                                                                                                                                                                              ; Score 365; DB 11;
; Pred. No. 4.4e-88;
0; Mismatches 0;
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100.0%;
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96US-00731499.
97US-00785532.
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 365; Conservative
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16-OCT-1996;
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The sequence is that of the genomic sequence of ZABC-1 (zinc finger amplified in breast cancer.) It maps to the core of the 20q13.2 amplicon and is overexpressed in primary tumours and breast cancer call lines having 20q13.2 amplification. The exact coding region for the genomic sequence is not given. The sequence can be used as a probe for the detection of chromosomal abnormalities at 20q13. It and other sequences is solated from the 20q13 amplicon are consistently amplified in primary tumours. These sequences are useful as probes or as probe targets for monitoring the relative copy number of corresponding sequences from a monitoring the relative copy number of corresponding sequences from a therapeutic applications for modulating the expression of the endogenous gene or the activity of the gene product. Examples of therapeutic applications for modulating the expression, gene therapy, approaches include antisense inhibition of gene expression, gene therapy, and monoclonal antibodies that specifically bind the gene products. The products can also be used in the treatment of other diseases, e.g. agerelated macular degeneration, Leber's congenital ammanosis and retinitis
                                                                                                          New sequences from the 20q13 amplicon - used for detecting chromosomal abnormalities, particularly tumours, and for developing products for treating diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10282 BP; 2820 A; 2222 C; 2191 G; 3047 T; 0 U; 2 Other;
                                                                                                                                                                                                                             Claim 1; Page 64-67; 91pp; English.
                          WPI; 1998-110587/10.
P-PSDB; AAW23975.
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10038 AGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTACTCTTGAATTCCTCAGTTCAAGA 10098 GATCCTTCTGCCTCAGCTTCCCAGGTACCTGAGACTATATGTCCTCCTACCATCCACAGC 10158 10159 TCATTTTTAAA-TTTTTTTTTTACAGATGGAGTTGCCCAGGCTCGTCTTGAACTCCTGGCC 10217 240 360 AGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGA 180 61 ATTCTTTTGATTTGTTTAGTCTTACTTTATTTTAGAGAAAGGGTCTTGCTCCGTCATCT 120 9 TTTGTGGTCCTCCAAGGCTTACTTAACTCTCTCCTTTAACTCTTAAACTCTCTATTTT TTTGTGGTCCTCCAAGGCTTAACTCTGTGGGTTTAACTCTTAACCCTGTGTATTTT GATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTGCTGCTACCATGCACAGC TGATTTTTAAATTTTTTTTTGTAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCC TGAGGTGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCAC 1; Gaps 89.3%; Score 325.8; DB 2; Length 10282; 17; Indels Pred. No. 1.2e-77; 0; Mismatches Query Match 89.3%; Best Local Similarity 95.1%; Matches 347; Conservative 121 9919 181 301 10039 241 9979 10099 d 셤 용 셤 g ઠે ò 8 ð ò

ABD32548 standard; DNA; 310268 BP. 10278 ĠĊŤTĠ 10282 GCTTG 365 361 10218 ABD32548; ABD32548
ID ABD3
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Human cancer-associated genomic DNA HD14-033.

(first entry)

18-NOV-2004

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contiguous nucleotides for an isolated nucleic acid sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the above included are an expression vector comprising the above comprising the above comprising the above comprising the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising the above polypeptide (any of the above polypeptide, a hybridoma that produces the above comprising to the above polypeptide, a hybridoma that produces the above polypeptide, a hybridoma that produces the above comprising the above polypeptide, a hybridoma that produces the above control and an isolated antibody, (or its antigen binding fragment) that comprising the above polypeptide, a hybridoma that produces the above control antibody a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above control and a pharmaceutical composition comprising the above control and a method for delivering growth of cancer cells in an individual, a method for their fragments), methods of screening in an individual, an electronic library comprising the above proved control contro The invention relates to an isolated nucleic acid comprising at least 10 New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer. 18 CTTACTTAACTCTGTGGGTTTAACTCTTAACCCTGTGTATTTTTATTCTTTTGATTTGTTT Sequence 310268 BP; 87522 A; 60932 C; 62901 G; 98913 T; 0 U; 0 Other; 40.4%; Score 147.6; DB 13; Length 310268; 65.7%; Pred. No. 4.1e-29; Human, ds, cancer-associated protein; gene; cytostatic; cancer; leukaemia; lymphoma; CAP. 0; Mismatches 114; at ftp.wipo.int/pub/published\_pct\_sequences Morris DW, Morris DW, Malandro MS; claim 16; seqid 24; 310pp; English. 14-MAR-2003; 2003US-00388838. 15-APR-2003; 2003US-00417375. 13-JUN-2003; 2003US-00461862. 15-SEP-2003; 2003US-00663431. 15-DEC-2003; 2003US-00737318 17-FEB-2004; 2004WO-US004730 (SAGR-) SAGRES DISCOVERY INC. Best Local Similarity 65.7 Matches 234; Conservative WPI; 2004-652914/63 WO2004074320-A2 Homo sapiens. 14-FEB-2003; 02-SEP-2004 Query Match ò

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                                                           78009
                                                                                                   78010 CTCCCAAGTAGCTGAGATTACAGGTGCCCACACTCTCAGATAATTTTTGTATTTTTA 78069
                                                                                                                                          78070 CTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAGTGAT 78129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel tumour suppressor gene, referred to as faint. The invention also relates to the field of cancer therapy and cancer diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an LMT. The present
                                                                                                                       TTGTAGAGATGG-----AGTTGCCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGAT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTC 194
                                                                                                                                                                         77950 TGCAGTCTTGGCTCACTGCATTCTTTGCATCCTGGGCTCAAGTGATTCTCGTGCCTCAGC
                                                                               AGTOTTACTTTATTTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGG
                                       TGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGC
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                                                                                                                                                               CCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCACGCTTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 50335 BP; 15699 A; 9846 C; 9072 G; 14424 T; 0 U; 1294 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a subject for the LMT.
                                                                                                                                                                                                                                                                                                                      human;
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                                                                                                                                                                                                                                                                                                                     gene; Lmt; cancer; therapy; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule, useful for screening presence of an aberration in a gene encoding an
                                                                                                                                                                                                                                                                                                  Human tumour suppressor gene, Lmt intron 1 DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 299-314; 373pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is human Lmt intron 1 DNA
                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                     DNA; 50335
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Best Local Similarity 74.5%;
Matches 213; Conservative
                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                            1280/c
AAD58280 standard;
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                                                                                                       35768 AGCCICCCAGGIAGCIGGGACIATAGGAGIGIGCIACCAIGCCIAGCIAAITITIAAATI 35709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel tumour suppressor gene, referred to as Limt. The invention also relates to the field of cancer therapy and cancer diagnostics. The nucleic acid molecule is useful for screening a subject for the presence of an aberration in a gene encoding an LMT. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;
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                                                                    TTTTTTGTAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 TTTAGTCTTACTTTATTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule, useful for screening a subject for the presence of an aberration in a gene encoding an LMT.
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                                                                                                                                                                                                                               CCGCCTTGGCCTCCCACAGTGCTGAGATTACAGACGTGAGCCACCA 35607
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                                                                                                                                                                                        CTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCA
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Pred. No. 4.8e-29;
0; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 226475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour suppressor gene,
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Best Local Similarity 74.5%;
Matches 213; Conservative (
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2000US - 0231243P

2000US - 0231414P

2000US - 0231414P

2000US - 02328BB

2000US - 02329BP

2000US - 023239P

2000US - 023424P

2000US - 023429P

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2000US-0249244P.
2000US-0249245P.
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   211085 CTTTGTTT----GTTATGTTGCCCAGGCTGGTCTCGAACTCCTGGGCTCAGGTGATCCAC 211030
                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25019
                                                      CTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0179065P.
2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
2000US-0190076P.
2000US-0190076P.
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2000US-021647P

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2000US-0217496P

2000US-0218290P

2000US-0218290P

2000US-022963P

2000US-022513P

2000US-0225213P

2000US-0225214P

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2000US-0225264P

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2000US-02526P

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2000US-0230438P.
2000US-0231242P.
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2000US-0226868P.
2000US-0227182P.
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2000US-0209467P.
2000US-0214886P.
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2000US-0229343P.
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                                                                                                                                                                                                                        (first entry)
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2000US-0231242P
2000US-0231243P
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16-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
conversation by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
couplincleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK6950 and AAM82169
represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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69.8%; Pred. No. 1.6e-29;
tive 0; Mismatches 84; Indels 10; Gaps
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         17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249309P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0249301P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025149P.
06-DEC-2000; 2000US-025149P.
06-DEC-2000; 2000US-025149P.
08-DEC-2000; 2000US-025149P.
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2000US-0251868P.
2000US-0251869P.
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2000US-0251990P.
2000US-0254097P.
2000US-0249264P
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08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0232080P.
14-SEP-2000; 2000US-0232308P.
14-SEP-2000; 2000US-023239BP.
14-SEP-2000; 2000US-023364PP.
25-SEP-2000; 2000US-023499BP.
25-SEP-2000; 2000US-02349BP.
25-SEP-2000; 2000US-0234617P.
25-SEP-2000; 
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17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For expression by rectifying mutations or deletions in a patient s genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) cuplancies may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polynucleotides may be used to prevent. Connects and cancer metastesses of haematopoietic-related diseases, especially cancer metastesses of haematopoietic-derived cells. AAK64703 connects and cancer metastesses of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       899 AATITITIAAAATITITIGIGGAGACAGGCICTITGCIGCCCCAGICTGGTCTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.2%; Score 146.6; DB 4; Length 1385; Best Local Similarity 69.8%; Pred. No. 1.6e-29; Matches 217; Conservative 0; Mismatches 84; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 33541; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1385 BP; 469 A; 278 C; 289 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SM
                                2000US - 0249299P
2000US - 0249300P
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2000US - 0251969P
2000US - 0251969P
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05-JAN-2001; 2001US-0259678P.
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                                17-NOV-2000;
17-NOV-2000;
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08-DEC-2000;
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1066 CTTGTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCTCACTCTGTTATCCAAG 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CTTTTGATTTGTTTAGTCTTTACTTTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGCCTGAGGTGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTC 354
                                                                                                                                                                                                                                            Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATG-TGCTGCTACCATGCACAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3019 BP; 833 A; 670 C; 785 G; 731 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145.2; DB 12; Length
Pred. No. 4.7e-29;
0; Mismatches 78; Indele
Sato H,
Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human oncosuppressive gene (DRAGO) fragment
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2097; 2449pp; English.
Otsuki T, Wakam
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВБ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.8%;
Best Local Similarity 71.8%;
Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of the invention.
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    Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1366 CACCACAC 1373
                                          Yamamoto J, Isono Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCACGC 362
                                                                                                                        WPI; 2004-535376/52
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                                                                                                                                                                   P-PSDB; ADQ67124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21891 CACCTGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCACCTG 21945
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Pred. No. 9.2e-29;
0; Mismatches 107; Indels
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Begin
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09-MAY-2003; 2003JP-00131392.
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Continuation (3 of 5) of AB
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Best Local 8
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ADQ64936
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                                                                                                                                                                                                                                                                                                   78
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ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum; ds.
                                                                                        oncosuppressive polypeptide, useful for preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                         449 ACAATCACAGCTTACTTTAGTCCTGACCTCCGAGCTCAATAATACTCTCCCCAGCC
                                                                                                                                                                                                                                                                                                                                                GTCTTACTTTATTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                            139 GTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCAGGTAGCTGAGACTATATGTG-CTGCTACCATGCACAGCTGATTTTTAAATTTTTT
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                The invention relates to oncosuppressive polypeptides and encoding polynuclectides. The oncosuppressive gene is involved in apoptotic process and is regulated by p53 and p73. The oncosuppressive polynuclectides are useful for preparing a medicament for treating tumour. The present sequence represents a human oncosuppressive gene (DRAGO) fragment, located upstream of the first exon
                                                                                                                                                                                                                               Sequence 10735 BP; 2720 A; 2485 C; 2630 G; 2900 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human digestive system antigen genomic sequence SEQ ID NO: 2568
                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                   Query Match 39.7%; Score 145; DB 8; Length 10735; Best Local Similarity 67.8%; Pred. No. 7.7e-29; Matches 234; Conservative 0; Mismatches 105; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCAC 357
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                                                                                                                           Claim 3; Page 34-37; 42pp; English
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10-JUL-2001; 2001IT-MI001465
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                                            Broggini M, D'incalci M
                     (NOVU-) NOVUSPHARMA SPA
                                                                  WPI; 2003-221715/21
                                                                                                    treating tumors
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79; DB 4;

Score 143.6; DB 4 Pred. No. 1.9e-28; 0; Mismatches 79

Query Match 39.3%; Best Local Similarity 71.6%; Matches 202; Conservative

Length 11216;

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8240 TTTGTTTGTTTTAGAGATAAGGTCCTGCTCTGTCACTCAGGCTAGAGTGCAGTGGTGCT

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TTACTTTATTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGGTGTA

The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention

Disclosure; SEQ ID NO 2568; 986pp; English.

Sequence 11216 BP; 3857 A; 1984 C; 1812 G; 3563 T; 0 U; 0 Other;

8061

8060 GTCTCACTGTGTTGCCCAGGCTGGTCTCGAACTTCTGGGCTCAAGCTGTCCTCCTGCCTT 8001

261 TAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGATCCTCCTGCGTT 320

202 CAGGIAGCIGAGACIAIAIGIGC-IGCIACCAIGCACAGCIGAIIIIIAAAIIIIIIG 260

8120

8180 Arcarecrecrecaecerdaacrecreascaecaecececerecaerec

142 ATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCC

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Ruben SM;
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02-0CT-2000; 20-0CT-2000; 20-0C
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17-NOV-2000; 2
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17-NOV-2000;
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17-NOV-2000;
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05-JAN-2001;
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Human; colon cancer; congenital abnormality; infection; colitis;
inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;
intestinal inflammatory disorder; malabsorption syndrome; gastric;
sigmoid disease; antibacterial; antiviral; antiinflammatory; cytostatic;
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                                                                               8000 AACCTTCCAAAATACTGGGATTACAGACATGAGCCACCACAC 7959
321 GACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCACGC 362
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2000US-018464P.
2000US-018974P.
2000US-0199076P.
2000US-0199123P.
2000US-029467P.
2000US-0204667P.
2000US-0214886P.
                                                                                                                                                                                                                                                                                  AAS39593 standard; DNA; 11216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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17-MAR-2000;
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28-JUN-2000;
30-JUN-2000;
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04-FEB-2000;
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19-MAY-2000;
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Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases.

WPI; 2001-502630/55

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2000US-0216647P

2000US-0217487P

2000US-0217487P

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2000US-0217487P

2000US-0229543P

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08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon including colon cancers and also for testing and detection e.g. diagnosis. S Ruben Barash SC, WPI; 2001-465567/50 ð Rosen

Disclosure; SEQ ID NO 490; 562pp; English

The present invention relates to the isolation of novel human colon associated polypeptides (AAU22468-AAU22701), and the CDNA and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the colon including colon cancer, congenital abnormalities (e.g. atreata and stenosis), bacterial and viral infections inflammatory bowel disease (IBB), neoplastic cell disorders (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, colonic inflammation, diarrhoea and

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2000US-0225757P-
2000US-0225758P-
2000US-022579P-
2000US-022679P-
2000US-022681P-
2000US-022681P-
2000US-0228924P-
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2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
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13-0CT-2000;
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  8181
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dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal obstruction and sigmoid diseases. The polynucleotides sequences of the invention can also be used in gene therapy. AAS19582-AAS4060 represent DNA sequences encoding for the novel human colon associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                           260
                                                                                                                                           TTACTTTATTTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGGTGTA 141
                                                                                                                                                              GTCTCACTGTGTTGCCCAGGCTGGTTGTCTCGGACTTCTGGGCTCAAGCTGTCCTCCTGCCTT
                                                                                                                                                                                   ATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCC
                                                                                                                                                                                                                           CAGGTAGCTGAGACTATATGTGC-TGCTACCATGCACAGCTGATTTTTAAATTTTTTTG
                                                                                                                                                                                                                                       TAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGATCCTCCTGCGTT
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; cancer; liver disorder; hepatitis; neural disorder; simer's disease; human; colon; ds.
                                                                                Sequence 11216 BP; 3857 A; 1984 C; 1812 G; 3563 T; 0 U; 0 Other;
                                                                                                   DB 5; Length 11216;
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                                                                                                   Score 143.6; DB 5; Length
Pred. No. 1.9e-28;
0; Mismatches 79; Indels
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                                                                                                                                                                                                                                                                                                          GACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCACGC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human novel colon related polypeptide DNA SEQ ID NO 490
                                                                                                                                                                                                                                                                                                                                                                                ADB32553 standard; DNA; 11216 BP
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2000US-020515P.
2000US-0214886P.
2000US-0214886P.
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2000US-0217496P.
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71.6%;
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Best Local Similarity 71.6
Matches 202; Conservative
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02-MAR-2000; 2
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11-MAR-2000; 2
11-MAY-2000; 2
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28-JUN-2000; 2
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07-JUL-2000; 2
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Alzheimer's
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82 TTACTTTATTTTTAGAGAAAGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGGTGTA 8240 rirreririeriririadadaraadericerierierierekoereaderideaderdeea

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142 ATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCC

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202 CAGGTAGCTGAGACTATATGTGC-TGCTACCATGCACAGCTGATTTTTAAATTTTTTTTG

8060 GTCTCACTGTGTTGCCCAGGCTGGTCTCGAACTTCTGGGCTCAAGCTGTCCTCCTGCCTT

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261 TAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGATCCTCCTGCGTT

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The invention relates to an isolated nucleic acid molecule encoding a polypeptide. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents a human novel colon related polypeptide DNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030050231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
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08-NOV-2000; 2000US-0246470P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246523P.
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08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024921P.
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17-NOV-20
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05-JAN-2001; 2001US-0259678P
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RUBEN S M.
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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27665.
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2000US-0184664P.
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19-MAY-2000;
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AAK72853/
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Sequence 11216 BP; 3857 A; 1984 C; 1812 G; 3563 T; 0 U; 0 Other;

39.3%; Score 143.6; DB 9; Length 11216;

Query Match

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5-SEP-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
couplement the patients own production of (I). Additionally, (I)
couplement the patients own production of (I). Additionally, (I)
couplement the patients own production of (I). Additionally, (I)
couplement the patients own production of (I). Additionally, (I)
couplement the patients and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
concers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK87950 and AAM82169
represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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Query Match 39.1%; Score 142.8; DB 4; Length 14540; Best Local Similarity 66.9%; Pred. No. 3.3e-28; Matches 222; Conservative 0; Mismatches 102; Indels 8;

8; Gaps

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274 GCCCAGGCTGGTCTTGAACTCCTGAGGTGATCCTCCTGCGTTGACCTCCCAAGTA 333
                                                                                         11892 GCTGGGATTACAGGCGTGAGGCACTTCGCTGG 11861
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APPLICANT: Collins, Collin
APPLICANT: Godfrey, Soo In
APPLICANT: Godfrey, Tony
APPLICANT: Godfrey, Tony
APPLICANT: Rowel, David
APPLICANT: Rowel, David
APPLICANT: Rowel, Johanna
ITILE OF INVENTION: GENES FROM THE 20013 AMPLICON AND THEIR USES
FILE REFERENCE: 2500.124US3
CURRENT APPLICATION NUMBER: US/08/892,695A
CURRENT FILING DATE: 1997-01-15
BARLIER FILING DATE: 1997-01-17
BARLIER FILING DATE: 1996-10-16
BARLIER APPLICATION NUMBER: 08/731,499
BARLIER APPLICATION NUMBER: 08/731,499
BARLIER APPLICATION NUMBER: 08/680,395
BARLIER PILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
                                                           Sequence Sequence
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US-09-949-016-157471
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US-09-949-016-89666
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US-09-949-016-89688
US-09-949-016-89688
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-09-949-016-121481
                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

**SOFFWARE: FREESEQ FOR Windows Version 4.0
10241 TGATTTTTAAATTTTTTTTTTGTAGAGATGGAGTTGCCCAGGCTGGTCTTGAACTCCTGGCC 10300
                                                                                                                                                 TGAGGTGATCCTCCTGCGTTGACTCCCAAGTATCTTAGACTACAGATGCACTCCACCAC 10360
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                                                                                                                                                                                                                                                                                                                    ; Sequence 12604, Application US/09949016; Patent No. 6812339
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Best Local Similarity 100.
Matches 365; Conservative
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ORGANISM: Human
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LENGTH: 20022
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RESULT 3

US-09-449-016-16004

i Sequence 16004, Application US/09949016

i Patent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

I CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PRILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 16004
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US-09-949-016-13150
is parent No. 681239
j GENERAL INFORMATION:
j PAPLICANT: VENTER, J. Craig et al.
itTILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
j CURRENT APPLICATION NUMBER: US/09/949,016
j CURRENT PILING DATE: 2000-04-14
j PRIOR APPLICATION NUMBER: 60/241,755
j PRIOR APPLICATION NUMBER: 60/217,768
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100.0%; Pred. No. 1.5e-100;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 365; Conservative
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US-09-94-016-17170

Sequence 17170, Application US/09949016

Sequence 17170, Application US/09949016

Sequence 17170, Application US/09949016

Sequence 17170, Application US/09949016

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      40 ACTCTTAACCCTGTGTATTTTATTCTTTTGATTTGTTTAGTCTTACTTTATTTTTAGAGA
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// OTHER INFORMATION: n = A,T,C or uS-09-949-016-17170
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASEEQ for Windows Version 4.0

SEQ ID NO 12675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5049 AAGGA-----TGCTGAGGCTGGTCTTGAACTCCTGGCATCAAGCAATCCTCCCGCCTTA 6102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5869 raarigririraagagacagggicicacricidricarrcagacrgaagrgcagrga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 TACTITATITITAGAGAAAGGGICTIGCICCGICATCIAGATIGGAGIGCAGCGGIGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 TCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGGTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 38538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 149.2; DB 4; Length
Pred. No. 8.1e-35;
0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13150
LENGTH: 38538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.09-949-016-12675
Sequence 12675, Application US/09949016
Patent No. 6812339
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(38538)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-13150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.4%;
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                                                                                                                         TYPE: DNA
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ORGANISM: Human
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US-09-949-016-16452
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                                                                                                                                                                                                                                                                                     US-09-949-016-51283
                                                                                                                                                                                                                                          TYPE: DNA
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US-09-949-016-15960/c

Sequence 15960, Application US/09949016

Sequence 15960, Application US/09949016

Sequence 15960, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISWS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15960
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Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
                         18090 AACCTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCCTCCCTGGTAGCTGAACCACAGGT 18031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17970 CCCAGGCTGGTCTTGAACTCCTGGGTTCCAGTGATCCTCCTGCCTCAGCCTCCTAGTAG 17911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18030 GCATGTCACCACCACCGGCTATTGCTTGTATTGTTGTAGAGACAAGGTCTCACTATGTTG 17971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 CCCAGGCTGGTCTTGAACTCCTGGCCTGAGGTGATCCTCCTGCGTTGACCTCCCAGTAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCCCCAGGTAGCTGAGACTATATGT
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                                                                                                                               134868 GGTGCTGGGATTACAGGTGTGAGCCACCGTGC 134899
                                                                                      331 GTATCTTAGACTACAGATGCACTCCACCACGC 362
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US-09-949-016-15960
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271
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Sequence 16452, Application US/09949016

Sequence 16452, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

PILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

PRICH REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/02/941,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

SOFTWARE: PSECIE OF WINDOWS Version 4.0

SEQ ID NO 16452

LENGTH: 52971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 CCCAGGTAGCTGAGACTATATGTG-CTGCTACCATGCACAGCTGATTTTTAAATTTTTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      406 CCCGAGTAGCTGAGATTACAGGTGCCCACCATGCCCGGCTAATTTTTGTATTTTTAG 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 TACTABATACTACCTTTTTCTTATGCABACTAGTATTTCABABATATCAGATTTCTTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.7%; Score 144.8; DB 4; Best Local Similarity 67.2%; Pred. No. 2.5e-34; Matches 238; Conservative 0; Mismatches 107;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR RILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 51283
LENGTH: 601
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| LCCATION: (1)...(52971)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16452
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Sequence 11950, Application US/09949016
; Sequence 11950, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, US. Craig et al.
; APPLICANT: VENTER, US. CRAIG et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPREMENT: 2000.1307
; CURRENT APLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; RRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESE for Windows Version 4.0
; SEQ ID NO 11950
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Patent No. 6812339;
GENERAL INFORMATION:
A PAPLICANT: VENATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                 TTTTGTAGAACAAGGTTTCCCCATGTTGCCCAGGCTGGTCTTGAACTCCTGGGCACAGG 49270
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49151 AGCCTCCCAAGTAGCTGGGACTACAGGTGTGTGCCACCATGCCCAGCTAATTTTTGTATT 49210
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                                                                                                                                                   TGATCCTCCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCACCACGCT 363
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US-09-949-016-13230/c
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US-09-949-016-11950
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APPLICAMT: VENTER, J. Craig et al.
TITLE OF INVENTON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTON: UNBER: US/09/949, 016
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESEE FOR WINDOWS VETSION 4.0
SEQ ID NO 15151
LENGTH: 73295
                                                                                                                                                                                                                                                         21406 CAGCAGGCAATCTTAGCTCACTGCAGCCTCCACCTCCTGGTTCAAACAATTCTCCTGC 21465
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Pred. No. 2.4e-33;
                            DB 4;
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                          Score 144.8; DB
Pred. No. 2e-33;
0; Mismatches 8
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15151
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Best Local Similarity
Matches 217; Conserva
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Best Local Similarity
Matches 212; Conserv
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Sequence 15090, Application US/09949016
| Sequence 15090, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICAMT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: US-0/241,755 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SSOTHARE: PSESEE FESTER FES
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Pred. No. 3e-33;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESCEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 13230
LENGTH: 121433
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67.2%;
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Best Local Similarity
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ORGANISM: Human
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ORGANISM:
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FACENT NO. 0812439;
FACENT NO. 08124309;
FACENTEAL TRFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR PELICATION NUMBER: 66/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 12351
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Pred. No. 1.9e-33;
0; Mismatches 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12351, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.4%;
Matches 207; Conservative 0
Matches 207; Conservative
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Sequence 121870, Application US/09949016
Sequence 121870, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TALE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 121870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 30, 2005, 05:17:39
Job time : 138 secs
US-09-949-016-121870/c
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US-09-949-016-121870
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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APPLICANT: GRAY, Joe W.
APPLICANT: GRAY, Joe W.
APPLICANT: HANG, Solin
APPLICANT: HONG, Solin
APPLICANT: KOMER, Joun
APPLICANT: KOMER, Joun
APPLICANT: ROWEN, Johanna
TITLE OF INVENTION: GENES FROM THE 20q13 AMPLICON AND THEIR
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,499
FILING DATE: 16-OCT-1996
US-10-027-632-46475
US-10-027-632-46475
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US-10-674-1244-25157
US-10-674-1244-25157
US-10-674-1244-25157
US-10-719-993-6815
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US-10-367-034-1176-03
US-10-119-993-6862
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Sequence 1708, Ap
Sequence 11, Appl
Sequence 195, Appl
Sequence 6876, Ap
Sequence 17560, A
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5169.324 Million cell updates/sec
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1 TITGIGGICCTCCAAGGCTT......GATGCACTCCACCACGCTTG 365
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8: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
10: /cgn2
                                                                                                                                                                                                            August 30, 2005, 03:59:23; Search time 462 Seconds
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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3 US-10-087-192-1708
1WS-10-428-489-11
9 US-10-367-094-195
1 US-10-719-993-6876
1 US-10-741-600-17560
1 US-10-741-600-17560
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB E
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PUblication No. US20040006780A1
GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA K.
APPLICANT: GERBER, HANS-PETER
TITLE OF INVENTION: VGEF-MODULATED GENES AND METHODS EMPLOYING THEM
FILE REFERENCE: 08800080-0102
CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT APPLICATION NUMBER: US/10/428,487
FRIOR APPLICATION NUMBER: 08/815,153
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PARCHAIN VET: 2.1
SEQ ID NO 11
LENGTH: 301692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73300 CTCTCATAGCATTATGGAAACAACTCGAATACAACTACGTCAATTATTCATCTTTTTTT
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Pred. No. 4.1e-30;
0; Mismatches 114; Indels 8; G
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0
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                                                                                                                                                                                             100.0%; Score 365; DB 13;
100.0%; Pred. No. 1.4e-91;
ive 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1708
LENGTH: 36022
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Best Local Similarity 65.7%;
Matches 234; Conservative
                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 365; Conservative
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ORGANISM: Homo sapiens
                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1708
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Sequence 1708, Application US/10087192

Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: Engelhard, Elic K.
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/0798,586

PRIOR PLILING DATE: 2000-01-01
PRIOR PLILING DATE: 2000-01-02
PRIOR PLILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic Sequence Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 365; DB 8; 100.0%; Pred. No. 8.7e-92;
                                                                                             NAME: Hunter, Tom.
RECISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 23070-068910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/680,395
FILING DATE: 15-UUL-1996
ATTORNEY/AGENT INFORWATION:
NAME: HUNCET, TOM
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..10365
OTHER INFORMATION: /note=
OTHER INFORMATION: ZABC1"
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Matches 365; Conservative
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73360 TITITITITITITITITIGAGACAGAGTCCCACTCCATCCAGGCTGGGTGCAGTGG 73419
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                                                                                                                                                   198 TICCCAGGIAGCIGAGACIAIAIGIGCIGCIACCAIGCACAGCIGAITITITAAAITITI 257
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                                                                TGTAATCATAGCTTACTGTAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGC 197
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                                                                                             18 CTTACTTAACTCTGTGGGGTTTAACTCTTAACCCTGTGTATTTTATTCTTTTGATTTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer FILE REPERENCE: 529452001500
CURRENT APPLICATION NUMBER: US/10/367,094
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 203
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-719-993-6876; Sequence 6876, Application US/10719993; Publication No. US20040265849A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 195, Application US/10367094
Publication No. US20040170982A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
US-10-367-094-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 195
LENGTH: 310268
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US-10-367-094-195
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// NAME/KEY: misc_feature
// LOCATION: (1) ... (414295)
// THER INTERMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-:
US-10-719-993-6876
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Publication No. US20050026169A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLO10499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT PILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17560

LENGTH: 209822
APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLEO FO INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6876
LENGTH: 414295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 40.3%; Score 147.2; DB 20; Length 414295; Best Local Similarity 70.6%; Pred. No. 6e-30; Matches 226; Conservative 1; Mismatches 84; Indels 9; G
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Pred. No. 5.9e-30;
0; Mismatches 92;
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Best Local Similarity 69.6%;
Matches 231; Conservative
                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERBUCE: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                              APPLICANT: Wang, David G. IILLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                        THILE COFINENTION: POLYMORPHISMS IN CHE HURS THE REPERRENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-24
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTERE FOR WINDOWS VERSION 4.0
SERNGTH: 437
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Publication No. US20020198371A1 GENERAL INFORMATION:
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                                                                                                                                                                         138374 CTCCACCTCCTGGGTTCAAGCAATTCTCCTGCCTTAGCCTCCCAAGTAGCTGGGACTATA 138433
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                                                                                138314 CAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGTGATCTCAGCTCACTGCAAC 138373
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                                                                                                                                          CTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 128, Application US/10417375
; Publication No. US20040219528A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer; TILE REFERENCE: 529401600
; CURRENT APPLICATION NUMBER: US/10/417,375
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.9%; Score 145.8; DB 20; Length Best Local Similarity 67.3%; Pred. No. 1.5e-29; Matches 239; Conservative 0; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138554 GGTGCTGGGATTACAGGTGTGAGCCACCGTGC 138585
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ORGANISM: Homo sapiens
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US-10-417-375-128
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RESULT 8 US-10-027-632-46474/c ; Sequence 46474, Application US/10027632

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US-10-027-632-46475/c
                                                                                                                                                                   TYPE: DNA
CRGANISM: Human
US-10-027-632-46474
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JERGERAL IN PROPERTION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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Pred. No. 1.2e-30;
1; Mismatches 97; Indels
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
SEQ ID NOS: 325720
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Best Local Similarity 68.4%;
Matches 232; Conservative
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US-10-027-632-46475
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j Sequence 44475, Application US/10027632

j Publication No. US20030204075A9

j GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1909-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FRAISE FRAISEO FOR Windows Version 4.0
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Pred. No. 1.2e-30;
1; Mismatches 97
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46474
LENGTH: 437
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Best Local Similarity 68.4%;
Matches 232; Conservative
                                                                                                                                                                                                    Query Match
Best Local Similarity 68.4%;
Matches 232; Conservative
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Best Local Similarity
Matches 234; Conserv
                                                                                                                                            RESULT 13
US-10-674-124A-25157
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                                                                                                                                                                                                                                                                                        260 CAGCCTCRACTTCCCAGGCTCAAGTGATCCTCCTGCCTTAGCCTCCCAAGTAGCTGGGAC 201
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                                                                          200 cacagecarecaccaccacrescrastririreraririridadadagacaeserring 141
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                                                                                                                                                                                                                                                       TAGTCTTGAATTCCTGAGTTCAAGAGATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGAC
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Pred. No. 5.7e-30;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 CCAAGTATCTTAGACTACAGATGCACTCCACCACGCTTG 365
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67.8%;
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Matches 234; Conservative
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ORGANISM: Homo sapiens
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US-10-483-241-5
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OTHER INFORMATION: Distance between a terminus base of telomere on OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base OTHER INFORMATION: sequence: 30892783

PEATURE: OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 120072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 TITITITIGIAGAGATGG-----AGITGCCCAGGCTGGTCTTGAACTCCTGGCCTGAG 304
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                                                                                                                                                                                                                       Sequence 25157, Application US/10674124A
Publication No. US20040197797A1
GENERAL INFORMATION:
APPLICANT: INOXO, Hidetoshi
APPLICANT: TAMIYA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORIN-003CIP
313 CCTGCGTTGACCTCCCAAGTATCTTAGACTACAGATGCACTCCAC 357
                                   FILE KEFEKENCE: OKINOUSCLE;
CURRENT PELLING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/27,511
PRIOR PELLING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2000-112699
PRIOR APPLICATION NUMBER: JP2002-327516
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR PILING DATE: 2002-09-28
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
SEROTH: 399
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OTHER INFORMATION: DISO7_00049858
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LOCATION: (1). .. (1980090)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
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US-10-741-600-17676/c
US-10-741-600-17676, Application US/10741600
; Sequence 17676, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; AFPLICANT: CARGILL, Michele et al.
; AFPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF; FILER REPERENCE: CL001499
; FILER REPERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: PSESEQ for Windows Version 4.0
; SEQ ID NO 17676
; LENGTH: 1980090
                                                                                                                                           Sequence 6815, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FASESEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 rgrgtattttattcttttgatttgtttagtcttactttattttagagaaagggtcttgc
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Pred. No. 1e-28;
0; Mismatches 87; Indels
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LENGTH: 1980090
365 G 365
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US-10-719-993-6815
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i LOCATION: (1)._.(1980090)
i OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-:
US-10-741-600-17676
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                                                                                                                                                                                                                                                                                                                                                                                                           180230 TCTGTCACCCAGGCTGGAGTGCAGGTGATCTCAGCTCACTGCAACCTCCACCTCCT 180171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180050 GCTGATCTTGAACTCCTGGGCTCAAATGATCCATTCACCTCAGCCTCCCAAAGTTCTGGG 179991
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                                                                                                                                                                                                                                                                     111 TCCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCT
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                                                                                                                                           Score 143.8; DB 21;
Pred. No. 1e-28;
                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                      Query Match
Best Local Similarity 69.8%;
Matches 227; Conservative
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
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AQ21795 HS. 178_B
BU076629 im50c03.y
BM452708 AGENCOURT
CN263690 170004241
BX411790 DKFZp686K
CK000205 AGENCOURT
CD65682 AGENCOURT
H73550 y810h07.r1
AW84134 QY3-OT906
BX641053 HOMO SAPI
CR749384 HOMO SAPI
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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9b htc:

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A1014798 CF9903.8 CR123312 K-EST0171 CA39823 C899911.X BM456792 AGENCOURT AA129746 zn91907.8 CD691041 EST7564 h A1590042 tr75c02.X BM044361 603621675 BG563044 602581828 AG145061 Pan trog1 AQ315924 RPC111-96 AQ315924 RPC111-96 AQ315924 AGENCOURT BC033208 Homo Sapi CN289800 170004243 B32496 HS-1015-B1- BF769916 RC3-IT001 AQ11520 CTT-HSP-2 AQ385850 RPC11-15 AQ749458 HS_5574_1	ALLIGNMENTS  ALLIGNMENTS  S11 bp DNA linear GSS 05-MAY-1999  HS_5077_A2_A10_SPGE RPCI-11 Human Male BAC Library Homo sapiens  GSG. A0512276 GSG. HOMO sapiens HOMO sapiens (SM Malacata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.  ENCAYOCA: Mesaca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.  ENCAYOCA: Malace, C., Mallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kaller, A., Shaker, R., Furiong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L., Shaker, R., Tarlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L., Shaker, R., Tarlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L. Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  Brock, Malairas GG, Wallace JC, Hood L.  Squance, Mathigton  University of Washington  University of Washi
A1014798 A1014798 CA398239 CA3982312 AA156792 AA1590042 AA56744561 BG563044 AQ315924 AQ315924 AQ315924 AQ315924 AQ315924 AQ315924 AQ315926 BC033208 CC899800 BC033208 CC899800 AQ311520 AQ311520 AQ311520 AQ311520 AQ311520	AQ512276  AG512276  AG51276  AG51276  AG51276  AG7  AG7  AG7  AG7  AG7  AG7  AG7  A
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Alo SP6E One Flates GI:47428 Ins (human) ns
66669999999999999999999999999999999999	AQ512276  By 5077 A2 A10 SP6E RPC  By 5077 A2 A10 SP6E RPC  AQ512276.1 GI:4742829  GSS. HOMO Sapiens (human)  HOMO Sapiens (human)  HOMO Sapiens (human)  HOMO Sapiens (human)  Homo Sapiens  Rallaryota; Matazoa; Ch  Mahairas, G.G., Mallace  Sequence-tagged connect  Contact: Malairas GG, W  High Troughput Sequence  Onloversity of Washingt  (10 Queen Anne Avenue I  Tel: (206) 616-3867  Email: jwallace@u.washingt  High Troughput Sequence  Clones are derived frog  Clones are derived frog  Ibrary availability, in  piecer@dejong.med.buf  BACPAC Resources (http  Clones are derived frog  Clones are derived frog  Seq Primer: SP6  Clones are derived frog  Location/Qual:  1. 511  Accanism="Hon Augies"
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137.8 137.8 137.6 137.6

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 2225)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Mooret, T. Marchana, K., Hong, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Mulaky, J.A., Gunaratne, P.H., Richards, S., Sanchez, A., Whiting, M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Halten, D., Ketteman, M., Madan, A., Rodung, A.C., Shevchenko, Y., Butterfield, Y.S., Katywinski, M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, A., Schein, J.B., Jones, S.J. and Marra, M.A., Schein, J.B., Jones, S.J. and Marra, M.A., Schein, J.B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC033179 2225 bp mRNA linear HTC 01-APR-2004 Homo sapiens ATPase, Class I, type 8B, member 3, mRNA (cDNA clone IMAGE:4581020), with apparent retained intron.
                                                                                                                                                                                                                                                                      168 CCTGAGTICAAGAGATCCTTCTGCCTCAGCTTCCCAGGTAGCTGAGACTATATGTG-CTG 226
                                                                                                                                                                                                                                                                                                                                    323 CCCGGGTTCAAGTGATTCTCCTGCCTCAGCTTCCCGAGTAGCTGGGGTTATAGGTGCCTC 264
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263 chaccacecceechaarrirrenarrirragiaeadacaeeerreecearecreecea 204
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Submitted (25-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                   108 TGCTCCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 GACTACAGATGCACTCCACCACGC 362
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC033179.1 GI:21619903
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Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
22709111
           Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TITGIGGTCCTCCAAGGCTTAACTCTGTGGGTTTAACTCTTAACCCTGTGTATTTT 109
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1 (Dases 1 to 751)
Volik,S. Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
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Pred. No. 3.7e-19;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                45.5%; Score 166; DB 8; Length 511; 100.0%; Pred. No. 4.8e-24; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
Tel: 415 502 7066
Fax: 415 502 5665
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Class: BAC ends.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MCF7_1-22F8"
/sex="female"
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BZ612069/c
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU076629 516 bp mRNA linear EST 27-AUG-2002 im50c03.yl HR85 islet Homo sapiens cDNA clone IMAGE:6038404 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 TTTCTATTTAGTTNTGTTTTGCTTTTGTTTTTGAGACAGAGTCTTGCTGTGTTGC 165
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 516)
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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                                                                       Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                    scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA
Tel: (206) 616-3618
Fax: (206) 616-3618
Email: Wallace@u.washington.edu
Sequence Tagged Connector
Plate: 2178 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=2178 Col=20 Row=B"
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Pred. No. 9.1e-19;
0; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 535.
Location/Qualifiers
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Best Local Similarity 70.1%;
Matches 216; Conservative
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  AUTHORS
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                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 43 Row: £ Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                       info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Peatherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ213795

HS_2178_B2_A10_MR_CIT_Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=20 Row=B, genomic survey
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
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                                                                                                                                                                                                                                                                                                                                                                                                                        This clone has the following problem: retained intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4581020"
/Lissue type="Eye, retinoblastoma"
/clone lib="NHH MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.8%; Score 141.6; DB 3;
larity 71.2%; Pred. No. 3.7e-19;
Conservative 0; Mismatches 79;
  Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .2225
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: poTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Homo sapiens
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218; Conserv
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AQ213795
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/clone lib="HR85 islet"
/clone lib="HR85 islet"
/note="Corgan: Pancreas, Vector: pBluescript SK(-); Site_1:
/note="Corgan: Pancreas, Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xhoi; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -lkb. 5,
Xhoi site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Buclid Ave., St.
Louis, MO 63110, E-mail: hinousedingate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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                                                                                                                                                                                                            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                           Fax: 617-495-8557
Email: dmelton@blobp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishkai, I., Scearce, M., Brestelli, J., Gradwolli, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardens, M., Glbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Badocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6038404"
/tissue_type="Purified pancreatic islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 468.
Location/Qualifiers
1. .516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
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RESULT 6 BM452708

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AGENCOURT 6401261 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5498573 57, mRNA Sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1000)
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/tissue_type="lymphoma, cell line"
/tasue_type="lymphoma, cell line"
/lab_host="DH10B [phage-resistant)"
/clone_lib="NHH MGC 85"
/note="Organ: lymph, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 AGGGTCTTGCTCCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bettp://image.llni.gov
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                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Brandenberger, R. Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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from undifferentiated hES cell lines H1 (p32), H7 and H9 (p26) maintained in feeder-free conditions"
17000424177371 GRN_ES Homo sapiens cDNA 5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
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Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="embryonic
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Geron Corporation
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CK000205

788 bp mRNA linear BST 26-NOV-2003
AGENCOURT 16363613 NIH MGC_220 Homo sapiens cDNA clone
IMAGE:30707474 5', mRNA sequence.
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                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 678)

Barr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.

EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5. sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKZZ), Email 8.wiemann@dKz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 81 sequence available.
This clone (DKZZp686K11227) is available at the RZPD in Berlin.
Please contact the RZPD Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GRRWANY; Email: clone@rzpd.de.
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/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTATTTTATTCTTTTGATTTGTTTTAGTCTTTATTTTTTAGAGAAAGGGTCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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Homo sapiens (human)
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Homo sapiens
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Best Local Similarity 69.0
Matches 223; Conservative
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/lab hose="Nature Road"
/lab hose="Nature Road"
/clone_lib="NIH MGC_220"
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/note="Organ: mixed; Vector: pyx-Asc; Site 1: EcoRI;
Site_2: NotI; Library is oligo-dT primed and directionally
cloned Denatured RNA was size fraction at 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according tomRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pyX-Asc vector. Average insert size
0.5-IKb. Adaptors 5'(AATTCGGCACAGGG]3' and 5'd
(CTCGTGCTGC)3'. 3' Linker sequence - GCGCCGCTGAGGCC T18.
Sequencing primers 5'(AATTCGCACAGGG)3' and 5'd
(CTCGTGCTG)3'. 3' Linker sequence - ECGGCCGCTGAGGCC T18.
Sequencing primers 3' end: T3 promoter primer 5'd
(TAATACGCTCACTAAAGGA)3'. 5' End: T7 promoter primer 5'd
(TAATACGCTCTAAAGGA)3'. Library was constructed in the
laboratory of M. Bento Soares. Average insert size 3-4kb
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                    Office of Cancer Genomics
National Cancer Institute / NIH
Badg. 31 Rm10A7 Detheada, MD 20892
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.MA.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plates: NDAM1072 row: c column: 03
High quality sequence stop: 675.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                      Contact: Daniela S. Gerhard, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gw.

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC c lone distribution information

can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDAM501 row: C column: 13
CD656882 837 bp mRNA linear EST 18-JUN-2003
AGENCOURT_14538022 NIA Human H1 Embryonic Stem Cell CDNA Library
(Long) Homo sapiens CDNA clone IMAGE:30422172 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                       GI:31898550
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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/mol_type="mRNA"
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                                                                                                                                                                       112 CCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCTG 171
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le, M., Chissoe,B., Moorris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Materston,R., Wilson,R., Materston,R., Wilson,R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
                            Length 837;
                            Score 139.4; DB 6; Length Pred. No. 1.2e-18; 0; Mismatches 91; Indels
                                                                                          GTGTATTTTATTCTTTTGATTTTGTTTAGTCTTACTTTATT
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Seq primer: M13RP1
High quality sequence stop: 368.
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69.0%;
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/organism="Homo sapiens"

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QV3-OT0065-290300-137-a06 OT0065 Homo sapiens CDNA, mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entrement as seen in the following URL
(http://www.ludwig.org.br.scripts/gethtml2.pl?tl=&t2=QV3-OT0065-290
300-137-a06&t3=2000-03-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence start: 10
Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone lib="Organ: ovary; Vector: puc18; Site_1: Smal; Site_2:
/note="Organ: ovary; Vector: puc18; Site_1: Smal; Site_2:
/mote="Organ: ovary; Vector: puc18; Site_1: Smal; Site_2: Smal; Vector: Smal; Vector: Smal; Site_2: Smal; Vector: Smal; 
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Homo sapiens mRNA; cDNA DKFZp686A24102 (from clone DKFZp686A24102).
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Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
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Submitted (13-JUL-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.9e-18;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                     Tel: +55-11-2704922
                                                                                                                                                           +55-11-2707001
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Homo sapiens mRNA; cDNA DKFZp686F02110 (from clone DKFZp686F02110).
CR749384
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686A24102) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686A24102 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
The German CDNA Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 TCCGTCATCTAGATTGGAGTGCAGCGGTGTAATCATAGCTTACTGTAGTCTTGAATTCCT
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/dev_stage="fetal"
/note="genomic"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 13-FEB-1999
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                                                                                            http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686F02110
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. I (basea I to 36) I Cararhini; Hominidae; Homo. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq33f08.xl Soares NhHMPu Sl Homo sapiens cDNA clone IMAGE:1934343
3' similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 831 Exror: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 253.
sequencing consortium of the German Genome Project. This clone (DKFZp686F02110) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please, contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                             organism="Homo sapiens"
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                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/done lib="Soares NhHMPu S1"
//done lib="Soares NhHMPu S1"
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
//pote="Organ: mixed (see below); Vector: pT7T3D-Pac
//pote="Organ: mixed modified polylinker; Site: 1: Not I;
Site 2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NDHPU, and fectal heart NDHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260212-265223,
340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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pregnant uterus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 138.4; DB 1; ilarity 73.4%; Pred. No. 2.3e-18; Conservative 0; Mismatches 66;
                                                 organism="Homo sapiens"
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Job time : 2202 secs
Location/Qualifiers
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